

SCORE Search Results Details for Appli

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10693629 and Search Result us-10-69
start

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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:34:25 ; Search time 25.6344 Seconds
(without alignments)
559.260 Million cell updates/sec

Title: US-10-693-629-48
Perfect score: 796
Sequence: 1 MDLMCKKMKHLWFFLLLVAA.....YFGWFDPWGQGLTVTVSSAS 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	687	86.3 147	2	S13519	Ig heavy chain V r
2	606	76.1 146	2	S09710	Ig heavy chain V r
3	600	75.4 155	2	S31511	Ig heavy chain - h
4	597	75.0 140	2	I37782	Ig variable region
5	597	75.0 155	2	S31512	Ig heavy chain - h
6	585.5	73.6 137	2	S31676	Ig heavy chain V r
7	584.5	73.4 139	2	S31586	Ig heavy chain V r
8	574	72.1 124	2	S31684	Ig heavy chain V r

SCORE Search Results Details for Appli

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10693629 and Search Result us-10-69
[start](#)

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OM protein - protein search, using sw model

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(without alignments)
559.260 Million cell updates/sec

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Perfect score: 796
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Post-processing: Minimum Match 0%
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2: pir2:*
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	Score	Match Length			
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2	606	76.1 146	2	S09710	Ig heavy chain V r
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7	584.5	73.4 139	2	S31586	Ig heavy chain V r
8	574	72.1 124	2	S31684	Ig heavy chain V r

SCORE Search Results Details for Application 10693629 and Search Result us-10-693-629-48.rup.

[Score Home Page](#)
[Retrieve Application List](#)
[SCORE System Overview](#)
[SCORE FAQ](#)
[Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10693629 and Search Result us-10-693-629-48.rup.

[start](#)

[Go Back to previous page](#)

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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:27:58 ; Search time 206.143 Seconds
(without alignments)
668.599 Million cell updates/sec

Title: US-10-693-629-48
Perfect score: 796
Sequence: 1 MDLMCKKMKHLWFFLLLVAA.....YFGWFDPWGQGTTLTVSSAS 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	674	84.7	492	2 Q7Z374_HUMAN	Q7z374 homo sapien
2	603.5	75.8	465	2 Q6GMX6_HUMAN	Q6gmx6 homo sapien
3	602.5	75.7	150	2 O95973_HUMAN	O95973 homo sapien
4	602	75.6	476	2 Q6GMX1_HUMAN	Q6gmx1 homo sapien

SCORE Search Results Details for Application 10693629 and Search Result us-10-693-629-49.rng.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10693629 and Search Result us-10-693-629-49.rng.

[start](#)

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2006, 23:21:08 ; Search time 435.692 Seconds
(without alignments)
7169.205 Million cell updates/sec

Title: US-10-693-629-49
Perfect score: 448
Sequence: 1 agatcttaagcaagtgtaac.....aggtggaaatcaaacgtacg 448

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

SCORE Search Results Details for Application 10 and Search Result us-10-693-629-49.rni

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10693629 and Search Result us-10-69 start

[Go Bac](#)

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2006, 23:51:15 ; Search time 132.431 Seconds
(without alignments)
6329.773 Million cell updates/sec

Title: US-10-693-629-49
Perfect score: 448
Sequence: 1 agatcttaagcaagtgtaac.....aggtggaaatcaaacgtacg 448

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query
No.	Score	Match Length DB ID Description

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

start

[Go Back to previous page](#)

OM protein - protein search, using sw model

Title: US-10-693-629-50
Perfect score: 670
Sequence: 1 MDMRVPAQLLGLLLLWLPGA.....OOFNSYPTFGOGTKVEIKRT 130

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      A_Geneseq_8:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
```

SUMMARIES

SCORE Search Results Details for Application 10 and Search Result us-10-693-629-50.rai

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10693629 and Search Result us-10-69
[start](#)

[Go Bac](#)

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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:40:49 ; Search time 34.0143 Seconds
(without alignments)
334.535 Million cell updates/sec

Title: US-10-693-629-50
Perfect score: 670
Sequence: 1 MDMRVPAQLLGLLLLWLPGA.....QQFNSYPTFGQGTKVEIKRT 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	602.5	89.9	236	2	US-09-859-053-30	Sequence 30, Appl
2	569.5	85.0	129	1	US-08-217-918-2	Sequence 2, Appli
3	558.5	83.4	129	2	US-09-019-441A-6	Sequence 6, Appli

SCORE Search Results Details for Application 10693629 and Search Result us-10-693-629-50.rapbm.

[Score Home](#) [Retrieve Application](#) [SCORE System](#) [SCORE](#) [Comments /](#)
[Page](#) [List](#) [Overview](#) [FAQ](#) [Suggestions](#)

This page gives you Search Results detail for the Application 10693629 and Search Result us-10-693-629-50.rapbm.

[start](#)

[Go Back to previous page](#)

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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:57:24 ; Search time 113.226 Seconds
(without alignments)
531.839 Million cell updates/sec

Title: US-10-693-629-50
Perfect score: 670
Sequence: 1 MDMRVPAQLLGLLLWLPGA.....QQFNSYPTFGQGTKVEIKRT 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

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SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						

SCORE Seal

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10693629 and Search Result us-10-69 start

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OM protein - protein search, using sw model

Run on: September 21, 2006, 01:34:25 ; Search time 22.3656 Seconds
(without alignments)
559.260 Million cell updates/sec

Title: US-10-693-629-50
Perfect score: 670
Sequence: 1. MDMRVPAQLLGLLLLWLPGA.....QQFNSYPTFGQGTKVEIKRT 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
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4: pir4:*

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SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	614.5	91.7	125	2	S40349	Ig kappa chain V-J
2	596.5	89.0	132	2	S40334	Ig kappa chain - h
3	596	89.0	117	2	S11700	Ig kappa chain pre
4	592.5	88.4	132	2	S38646	Ig kappa chain V r
5	586.5	87.5	128	2	S46372	IG light chain var
6	579.5	86.5	125	2	S40333	Ig kappa chain V-J
7	574.5	85.7	141	2	A49134	Ig kappa chain V-I
8	571.5	85.3	127	2	S11240	Ig kappa chain V r

This page gives you Search Results detail for the Application 10693629 and Search Result [us-10-69 start](#)

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2	596.5	89.0	132	2	S40334	Ig kappa chain - h
3	596	89.0	117	2	S11700	Ig kappa chain pre
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6	579.5	86.5	125	2	S40333	Ig kappa chain V-J
7	574.5	85.7	141	2	A49134	Ig kappa chain V-I
8	571.5	85.3	127	2	S11240	Ig kappa chain V r

SCORE Search Results Details for Application 10693629 and Search Result us-10-693-629-50.rup.

[Score Home Page](#)
[Retrieve Application List](#)
[SCORE System Overview](#)
[SCORE FAQ](#)
[Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10693629 and Search Result us-10-693-629-50.rup.

[start](#)

[Go Back to previous page](#)

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OM protein - protein search, using sw model ..

Run on: September 21, 2006, 01:27:58 ; Search time 179.857 Seconds
(without alignments)
668.599 Million cell updates/sec

Title: US-10-693-629-50
Perfect score: 670
Sequence: 1 MDMRVPAQLLGLLLWLPGA.....QQFNSYPTFGQGTKVEIKRT 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

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Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

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SUMMARIES

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2	601.5	89.8	236	2 Q6GMW1_HUMAN	Q6gmw1 homo sapien
3	592.5	88.4	236	2 Q6GMX8_HUMAN	Q6gmx8 homo sapien
4	590.5	88.1	236	2 Q6PIH7_HUMAN	Q6pih7 homo sapien